

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/541,086  
Source: Pg 110  
Date Processed by STIC: 7/12/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 07/12/2005

PATENT APPLICATION: US/10/541,086

TIME: 09:58:31

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\07122005\J541086.raw

3 <110> APPLICANT: Gallaher, Timothy K  
 5 <120> TITLE OF INVENTION: SECRETED PROTEIN FACTOR AND CELL MEMBRANE-BOUND SPLICE  
 VARIANT  
 7 <130> FILE REFERENCE: pct.001  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/541,086  
 C--> 10 <141> CURRENT FILING DATE: 2005-06-29  
 12 <150> PRIOR APPLICATION NUMBER: 60/438,059  
 13 <151> PRIOR FILING DATE: 2003-01-02  
 15 <160> NUMBER OF SEQ ID NOS: 30  
 17 <170> SOFTWARE: PatentIn version 3.2  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 254  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Homo sapiens  
 24 <400> SEQUENCE: 1  
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 27 1 5 10 15  
 30 Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Ala  
 31 20 25 30  
 34 Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu Gly Glu Ala  
 35 35 40 45  
 38 Cys Gly Thr Val Gly Leu Leu Glu His Ser Phe Glu Ile Asp Asp  
 39 50 55 60  
 42 Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu Trp Asn Gln Gln Asp  
 43 65 70 75 80  
 46 Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly  
 47 85 90 95  
 50 Arg Leu Arg Asp Val Ala Ala Leu Asn Gly Leu Tyr Arg Val Arg Ile  
 51 100 105 110  
 54 Pro Arg Arg Pro Gly Ala Leu Asp Gly Leu Glu Ala Gly Gly Tyr Val  
 55 115 120 125  
 58 Ser Ser Phe Val Pro Ala Cys Ser Leu Val Glu Ser His Leu Ser Asp  
 59 130 135 140  
 62 Gln Leu Thr Leu His Val Asp Val Ala Gly Asn Val Val Gly Val Ser  
 63 145 150 155 160  
 66 Val Val Thr His Pro Gly Gly Cys Arg Gly His Glu Val Glu Asp Val  
 67 165 170 175  
 70 Asp Leu Glu Leu Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr  
 71 180 185 190  
 74 Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu  
 75 195 200 205  
 78 Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala  
 79 210 215 220  
 82 Lys Tyr Trp His Ile Ile Leu Gly Gly Ala Val Leu Leu Thr Ala Leu

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83 225          230          235          240
86 Arg Pro Ala Ala Pro Gly Pro Ala Pro Pro Pro Gln Glu Ala
87          245          250
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 254
92 <212> TYPE: PRT
93 <213> ORGANISM: Mus musculus
95 <400> SEQUENCE: 2
97 Met Val Ala Ala Gly Ala Gly Val Thr Arg Leu Leu Val Leu Leu Leu
98 1          5          10          15
101 Met Val Ala Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Val
102          20          25          30
105 Gly Ala Ser Ala Arg Gly Thr Gly Ala Asp Gly Arg Glu Ala Glu Gly
106          35          40          45
109 Cys Gly Thr Val Ala Leu Leu Leu Glu His Ser Phe Glu Leu Gly Asp
110          50          55          60
113 Gly Ala Asn Phe Gln Lys Arg Gly Leu Leu Leu Trp Asn Gln Gln Asp
114 65          70          75          80
117 Gly Thr Leu Ser Ala Thr Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly
118          85          90          95
121 Arg Leu Arg Asp Val Ala Ala Val Asn Gly Leu Tyr Arg Val Arg Val
122          100          105          110
125 Pro Arg Arg Pro Gly Thr Leu Asp Gly Ser Glu Ala Gly Gly His Val
126          115          120          125
129 Ser Ser Phe Val Pro Ala Cys Ser Leu Val Glu Ser His Leu Ser Asp
130          130          135          140
133 Gln Leu Thr Leu His Val Asp Val Ala Gly Asn Val Val Gly Leu Ser
134 145          150          155          160
137 Val Val Val Tyr Pro Gly Gly Cys Arg Gly Ser Glu Val Glu Asp Glu
138          165          170          175
141 Asp Leu Glu Leu Phe Asn Thr Ser Val Gln Leu Arg Pro Pro Ser Thr
142          180          185          190
145 Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu
146          195          200          205
149 Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala
150          210          215          220
153 Lys Tyr Trp His Leu Ile Leu Gly Gly Ala Val Leu Leu Thr Ala Leu
154 225          230          235          240
157 Arg Pro Ala Ala Pro Gly Pro Ala Pro Ala Pro Thr Glu Ala
158          245          250
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 262
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 3
168 Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu Leu
169 1          5          10          15
172 Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Ala
173          20          25          30

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176 Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu Gly Glu Ala
177          35          40          45
180 Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe Glu Ile Asp Asp
181          50          55          60
184 Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu Trp Asn Gln Gln Asp
185 65          70          75          80
188 Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly
189          85          90          95
192 Arg Leu Arg Asp Val Ala Ala Leu Asn Gly Leu Tyr Arg Val Arg Ile
193          100          105          110
196 Pro Arg Arg Pro Gly Ala Leu Asp Gly Leu Glu Ala Gly Gly Tyr Val
197          115          120          125
200 Ser Ser Phe Val Pro Ala Cys Ser Leu Val Glu Ser His Leu Ser Asp
201          130          135          140
204 Gln Leu Thr Leu His Val Asp Val Ala Gly Asn Val Val Gly Val Ser
205 145          150          155          160
208 Val Val Thr His Pro Gly Gly Cys Arg Gly His Glu Val Glu Asp Val
209          165          170          175
212 Asp Leu Glu Leu Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr
213          180          185          190
216 Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu
217          195          200          205
220 Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala
221          210          215          220
224 Lys Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
225 225          230          235          240
228 Gly Ala Pro Asp Ala Gly Gly Gln Gly Gly Gly Gly Gly Gly Gly
229          245          250          255
232 Gly Gly Gly Ser Gly Arg
233          260
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 258
238 <212> TYPE: PRT
239 <213> ORGANISM: Mus musculus
241 <400> SEQUENCE: 4
243 Met Val Ala Ala Gly Ala Gly Val Thr Arg Leu Leu Val Leu Leu Leu
244 1          5          10          15
247 Met Val Ala Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Val
248          20          25          30
251 Gly Ala Ser Ala Arg Gly Thr Gly Ala Asp Gly Arg Glu Ala Glu Gly
252          35          40          45
255 Cys Gly Thr Val Ala Leu Leu Leu Glu His Ser Phe Glu Leu Gly Asp
256          50          55          60
259 Gly Ala Asn Phe Gln Lys Arg Gly Leu Leu Leu Trp Asn Gln Gln Asp
260 65          70          75          80
263 Gly Thr Leu Ser Ala Thr Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly
264          85          90          95
267 Arg Leu Arg Asp Val Ala Ala Val Asn Gly Leu Tyr Arg Val Arg Val
268          100          105          110

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271 Pro Arg Arg Pro Gly Thr Leu Asp Gly Ser Glu Ala Gly Gly His Val
272      115      120      125
275 Ser Ser Phe Val Pro Ala Cys Ser Leu Val Glu Ser His Leu Ser Asp
276      130      135      140
279 Gln Leu Thr Leu His Val Asp Val Ala Gly Asn Val Val Gly Leu Ser
280 145      150      155      160
283 Val Val Val Tyr Pro Gly Gly Cys Arg Gly Ser Glu Val Glu Asp Glu
284      165      170      175
287 Asp Leu Glu Leu Phe Asn Thr Ser Val Gln Leu Arg Pro Pro Ser Thr
288      180      185      190
291 Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu
292      195      200      205
295 Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala
296      210      215      220
299 Lys Tyr Trp Met Tyr Ile Pro Val Val Leu Phe Leu Met Met Ser
300 225      230      235      240
303 Gly Ala Pro Asp Ala Gly Gly Gln Gly Gly Gly Gly Gly Gly Ser
304      245      250      255
307 Ser Arg
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 1962
313 <212> TYPE: DNA
314 <213> ORGANISM: Homo sapiens
317 <220> FEATURE:
318 <221> NAME/KEY: CDS
319 <222> LOCATION: (47)..(811)
321 <400> SEQUENCE: 5
322 ggctcttggc tcacagccgt cccttcgctg gtgggaagaa gccgag atg gcg gca      55
323                                     Met Ala Ala
324                                     1
326 gcc agc gct ggg gca acc cgg ctg ctc ctg ctc ttg ctg atg gcg gta      103
327 Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu Met Ala Val
328      5      10      15
330 gca gcg ccc agt cga gcc cgg ggc agc ggc tgc cgg gcc ggg act ggt      151
331 Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Ala Gly Thr Gly
332 20      25      30      35
334 gcg cga ggg gct ggg gcg gaa ggt cga gag ggc gag gcc tgt ggc acg      199
335 Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu Gly Glu Ala Cys Gly Thr
336      40      45      50
338 gtg ggg ctg ctg ctg gag cac tca ttt gag atc gat gac agt gcc aac      247
339 Val Gly Leu Leu Leu Glu His Ser Phe Glu Ile Asp Asp Ser Ala Asn
340      55      60      65
342 ttc cgg aag cgg ggc tca ctg ctc tgg aac cag cag gat ggt acc ttg      295
343 Phe Arg Lys Arg Gly Ser Leu Leu Trp Asn Gln Gln Asp Gly Thr Leu
344      70      75      80
346 tcc ctg tca cag cgg cag ctc agc gag gag gag cgg ggc cga ctc cgg      343
347 Ser Leu Ser Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly Arg Leu Arg
348      85      90      95
350 gat gtg gca gcc ctg aat ggc ctg tac cgg gtc cgg atc cca agg cga      391

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351 Asp Val Ala Ala Leu Asn Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg
352 100          105          110          115
354 ccc ggg gcc ctg gat ggc ctg gaa gct ggt ggc tat gtc tcc tcc ttt      439
355 Pro Gly Ala Leu Asp Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe
356          120          125          130
358 gtc cct gcg tgc tcc ctg gtg gag tgc cac ctg tgc gac cag ctg acc      487
359 Val Pro Ala Cys Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr
360          135          140          145
362 ctg cac gtg gat gtg gcc ggc aac gtg gtg ggc gtg tgc gtg gtg acg      535
363 Leu His Val Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr
364          150          155          160
366 cac cct ggg ggc tgc cgg ggc cat gag gtg gag gac gtg gac ctg gag      583
367 His Pro Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu
368          165          170          175
370 ctg ttc aac acc tgc gtg cag ctg cag ccg ccc acc aca gcc cca ggc      631
371 Leu Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
372 180          185          190          195
374 cct gag acg gcg gcc ttc att gag cgc ctg gag atg gaa cag gcc cag      679
375 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala Gln
376          200          205          210
378 aag gcc aag aac ccc cag gag cag aag tcc ttc ttc gcc aaa tac tgg      727
379 Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys Tyr Trp
380          215          220          225
382 cac atc atc ctg ggg ggg gcc gtg ttg ctc aca gcc ctg cgt cct gct      775
383 His Ile Ile Leu Gly Gly Ala Val Leu Leu Thr Ala Leu Arg Pro Ala
384          230          235          240
386 gcg cca ggg ccc gcg cca ccg cca cag gag gcc tga tggatgtaca      821
387 Ala Pro Gly Pro Ala Pro Pro Pro Gln Glu Ala
388          245          250
390 tcattcccgt cgtcctgttc ctcatgatgt caggagcgcc agacgccggg ggccagggtg      881
392 ggggtggggg tgggggtggt ggtgggggta gtggccgggt agggcccagg ctggtcagcg      941
394 tcccgctctt cacaccagg ggcctccctt tctgctggag tccctgtgt cctcagccat      1001
396 cccaagaagg gtttgctagt cctcctttc ccccgctccc acgaggccac ctgggcccagc      1061
398 ccttgtcct ctgccttctg ctggcagagg agcagctgga ctggggcctt tggcacagca      1121
400 gccggtgtct cctgcgcccg cctcccccat ggccccatgc agccccaggg gcttccaccc      1181
402 tgcccatgga gtagagcccg agatcctggc cactatgcca gttctgacct cgcaccccc      1241
404 taccgccagc ccatgcagtc tgggaacatg ccgccttctc tccagcctct gtgcctttgt      1301
406 tccaggtggt ctaccctcc tgtccttggc tgggctaggt ggtcctgtcc aggcctctgc      1361
408 agcgcccccc tcactttgac actggactag gatgcagcct ccttctgtg tcccttgag      1421
410 ggtaccctgg gtccctcat caggggcaga ggcataaaag agtcggggct ggatggccgg      1481
412 gggcttctgg gcccgatgcc tagtgcagcc actggggtcg tggtttgaca tttgtctgcc      1541
414 tgggtgaaac aaggaatcct tgcctttaag gtgacaggcc ctccacaggc ttccagactt      1601
416 gaaggaaaag gtttaagaaa gaaaacaaaa ccaacagtta gtggagtcaa agcccagaca      1661
418 ctgtaaataa aacccctcc accaccccc gccgcccagc atcctacctg gactgcggtg      1721
420 ctacgagggc ctgcgggctt ttgctgtgtg ccaccctccc tgtaagtcta tttaaaaaca      1781
422 tcgacgatac attgaaatgt gtgaacgttt tgaaaagcta cagcttcag cagccaaaag      1841
424 caactgttgt tttggcaaga cggctctgat gtacaagctt gattgaaatt cactgctcac      1901
426 ttgatacggt attcagaaac ccaaggaatg gctgtcccca tctcatgtg gctgtgtgga      1961
428 g

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**VERIFICATION SUMMARY**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date